



SEQUENCE LISTING

<110> Dale Umetsu
Rosemarie DeKruyff
Jennifer McIntire
Gordon Freeman

<120> T CELL REGULATORY GENES ASSOCIATED WITH
IMMUNE DISEASE

<130> STAN-235CIP

<150> 60/302,344
<151> 2001-06-29

<150> 10/188,012
<151> 2002-07-01

<160> 53

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 305
<212> PRT
<213> M. musculus

<220>
<221> VARIANT
<222> (1)...(305)
<223> TIM-1 BALB/c allele

<400> 1
Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Pro
1 5 10 15
Gly Thr Val Asp Ser Tyr Val Glu Val Lys Gly Val Val Gly His Pro
20 25 30
Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr
35 40 45
Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu
50 55 60
Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr
65 70 75 80
Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
85 90 95
Asn Ser Val Glu Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile
100 105 110
Pro Gly Trp Phe Asn Asp Gln Lys Val Thr Phe Ser Leu Gln Val Lys
115 120 125
Pro Glu Ile Pro Thr Arg Pro Pro Thr Arg Pro Thr Thr Thr Arg Pro
130 135 140
Thr Ala Thr Gly Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val
145 150 155 160
Pro Thr Ser Ile Arg Val Ser Thr Ser Thr Pro Pro Thr Ser Thr His
165 170 175
Thr Trp Thr His Lys Pro Glu Pro Thr Thr Phe Cys Pro His Glu Thr
180 185 190
Thr Ala Glu Val Thr Gly Ile Pro Ser His Thr Pro Thr Asp Trp Asn
195 200 205
Gly Thr Val Thr Ser Ser Gly Asp Thr Trp Ser Asn His Thr Glu Ala

210	215	220
Ile Pro Pro Gly Lys Pro Gln Lys Asn Pro Thr Lys Gly Phe Tyr Val		
225	230	235 240
Gly Ile Cys Ile Ala Ala Leu Leu Leu Leu Leu Val Ser Thr Val		
245	250	255
Ala Ile Thr Arg Tyr Ile Leu Met Lys Arg Lys Ser Ala Ser Leu Ser		
260	265	270
Val Val Ala Phe Arg Val Ser Lys Ile Glu Ala Leu Gln Asn Ala Ala		
275	280	285
Val Val His Ser Arg Ala Glu Asp Asn Ile Tyr Ile Val Glu Asp Arg		
290	295	300
Pro		
305		

<210> 2
<211> 918
<212> DNA
<213> Mus musculus

<400> 2

atgaatcaga ttcaagtctt catttcaggc ctcataactgc ttctccagg cactgtggat	60
tcttatgtgg aagtaaaggg ggttagtggt caccctgtca cacttccatg tacttactca	120
acatatcgta gaatcacacaac gacatgttgg gcgcgagggc aatgcccatc ttctgcttgt	180
caaaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcggtag	240
aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgtttag	300
agtgacagtg gtctgttattt ttgtcgagtg gagattcctg gatgtttaa tgatcagaaa	360
gtgacctttt cattgcaagt taaaccagag attcccacac gtcctccaac aagacccaca	420
actacaaggc ccacagctac aggaagaccc acgactatt caacaagatc cacacatgt	480
ccaacatcaa tcagagtctc tacctccact cctccaaacat ctacacacac atggactcac	540
aaaccagaac ccactacatt ttgtccccat gagacaacag ctgaggtgac aggaatccca	600
tccctatactc ctacagactg gaatggact gtgacatcct caggagatac ctggagtaat	660
cacactgaag caatccctcc agggaaagccg cagaaaaacc ctactaaggg cttctatgtt	720
ggcatctgca tcgcagccct gctgtactg ctccttgtga gcaccgtggc tatcaccagg	780
tacatactta taaaaaggaa gtcagcatct ctaagcgtgg ttgccttccg tgtctctaag	840
attgaagctt tgcagaacgc agcggttgtg cattcccgag ctgaagacaa catctacatt	900
gttgaagata gacccatga	918

<210> 3
<211> 282
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(282)
<223> TIM-1, C.D2 ES-HBA and DBA/2J allele

<400> 3

Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Pro	
1 5 10 15	
Gly Ala Val Asp Ser Tyr Val Glu Val Lys Gly Val Val Gly His Pro	
20 25 30	
Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr	
35 40 45	
Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu	
50 55 60	
Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr	
65 70 75 80	
Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu	
85 90 95	

Asn	Ser	Val	Glu	Ser	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Arg	Val	Glu	Ile
			100					105				110			
Pro	Gly	Trp	Phe	Asn	Asp	Gln	Lys	Val	Thr	Phe	Ser	Leu	Gln	Val	Lys
			115					120				125			
Pro	Glu	Ile	Pro	Thr	Arg	Pro	Pro	Arg	Arg	Pro	Thr	Thr	Thr	Arg	Pro
			130				135				140				
Thr	Ala	Thr	Gly	Arg	Pro	Thr	Thr	Ile	Ser	Thr	Arg	Ser	Thr	His	Val
			145				150				155			160	
Pro	Thr	Ser	Thr	Arg	Val	Ser	Thr	Ser	Thr	Pro	Pro	Thr	Ser	Thr	His
				165				170				175			
Thr	Trp	Thr	His	Lys	Pro	Asp	Trp	Asn	Gly	Thr	Val	Thr	Ser	Ser	Gly
				180				185				190			
Asp	Thr	Trp	Ser	Asn	His	Thr	Glu	Ala	Ile	Pro	Pro	Gly	Lys	Pro	Gln
				195				200				205			
Lys	Asn	Pro	Thr	Lys	Gly	Phe	Tyr	Val	Gly	Ile	Cys	Ile	Ala	Ala	Leu
				210				215				220			
Leu	Leu	Leu	Leu	Leu	Val	Ser	Thr	Val	Ala	Ile	Thr	Arg	Tyr	Ile	Leu
				225				230				235			240
Met	Lys	Arg	Lys	Ser	Ala	Ser	Leu	Ser	Val	Val	Ala	Phe	Arg	Val	Ser
					245				250				255		
Lys	Ile	Glu	Ala	Leu	Gln	Asn	Ala	Ala	Val	Val	His	Ser	Arg	Ala	Glu
					260				265				270		
Asp	Asn	Ile	Tyr	Ile	Val	Glu	Asp	Arg	Pro						
				275				280							

<210> 4

<211> 849

<212> DNA

<213> Mus musculus

<400> 4

atgaatcaga	ttaaagtctt	catttcaggc	ctcataactgc	ttctccagg	cgctgtggat	60
tcttatgtgg	aagtaaaaggg	ggtgtgggt	caccctgtca	cacttccatg	tacttactca	120
acatatcgtg	gaatcacacaac	gacatgttg	ggccgagggc	aatgcccac	ttctgcttgt	180
caaaaatacac	ttatttggac	caatggacat	cgtgtcacct	atcagaagag	cagtcggtag	240
aacttaaagg	ggcatatattc	agaaggagat	gtgtccttga	cgatagagaa	ctctgttgag	300
agtgacagtg	gtctgtattt	ttgtcgagtg	gagattcctg	gatgtttaa	tgatcagaaa	360
gtgaccttt	cattgcaagt	taaaccagag	attcccacac	gtcctccaag	aagacccaca	420
actacaaggc	ccacagctac	aggaagaccc	acgactattt	caacaagatc	cacacatgt	480
ccaaacatcaa	ccagagtctc	tacccact	cctccaaacat	ctacacacac	atggactcac	540
aaaccagact	ggaatggcac	tgtgacatcc	tcaggagata	cctggagtaa	tcacactgaa	600
gcaatccctc	cagggaaagcc	gcagaaaaac	cctactaagg	gtttctatgt	tggcatctgc	660
atcgcgcccc	tgcgtctact	gctccctgt	agcaccgtgg	ctatcaccag	gtacatactt	720
atgaaaagga	agtcaagcattc	tctaagcgt	gttgccttcc	gtgtctctaa	gattgaagct	780
ttgcagaacg	cagcggttgt	gcattcccg	gctgaagaca	acatctacat	tgttgaagat	840
						849

<210> 5

<211> 305

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-2 BALB/c allele

<400> 5

Met	Asn	Gln	Ile	Gln	Val	Phe	Ile	Ser	Gly	Leu	Ile	Leu	Leu	Pro
1				5				10				15		

Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
 20 25 30
 Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
 35 40 45
 Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
 50 55 60
 Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
 65 70 75 80
 Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
 85 90 95
 Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
 100 105 110
 Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
 115 120 125
 Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
 130 135 140
 Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
 145 150 155 160
 Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
 165 170 175
 Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
 180 185 190
 Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
 195 200 205
 Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
 210 215 220
 Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
 225 230 235 240
 Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
 245 250 255
 Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
 260 265 270
 Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
 275 280 285
 Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
 290 295 300
 Ser
 305

<210> 6
 <211> 958
 <212> DNA
 <213> Mus musculus

<400> 6

```

aagctacggc tcttcctaa ctggcgtac catgaatcag attcaagtct tcatttcagg 60
cctcatactg cttctcccg gtgcgttga gtctcataca gcagtgcagg ggctggccgg 120
tcaccctgtc acacttccat gtatttattc gacacacctt ggtgaatcg ttccatatgtg 180
ttggggctta gggaatgcc gccattctt ttgtatacgg tcacttatct ggaccaatgg 240
atatacggtc acacatcaga ggaacagtgc ataccagcta aagggaaata tttcagaagg 300
aaatgtgtcc ttgaccatag agaacactgt tgtgggtat ggtgtccct attgctgtgt 360
agtggagata cctggagcgt tccattttgt ggactatatg ttgaaagtta aaccagaaat 420
ttccacaggt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
atccacacat gtaccaacat caaccagagt ctctacacctt acttctccaa caccagcaca 540
cacagagacc tacaaccagg aggccactac attttatcca gatcagacta cagctgaggt 600
gacagaaacc ttaccctcta ctcctgcaga ctggcataac actgtgacat cctcagatga 660
cccttggat gataacactg aagtaatccc tccacagaag ccacagaaaa acctgaataa 720
ggcttctat gtggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780
ggttatcacc aggtacgtgg ttatgaaaag gaagtcagaa tctctgagct ttgtgcctt 840
ccctatctt aagattggag cttcccccaa aaaagtggc gatgtgaaga 900
  
```

ccaggtctac attattgaag acactcctta ccctgaagaa gagtcctagt gcctctac 958

<210> 7
<211> 305
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(305)
<223> TIM-2, C.D2 ES-HBA and DBA/2J allele

<400> 7
Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Pro
1 5 10 15
Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
20 25 30
Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
35 40 45
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
50 55 60
Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
65 70 75 80
Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
85 90 95
Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
100 105 110
Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
115 120 125
Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
130 135 140
Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
145 150 155 160
Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
165 170 175
Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
180 185 190
Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
195 200 205
Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
210 215 220
Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
225 230 235 240
Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
245 250 255
Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
260 265 270
Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
275 280 285
Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
290 295 300
Ser
305

<210> 8
<211> 958
<212> DNA
<213> Mus musculus

<400> 8

aagctacggc tctctcctaa ctggtcgtac catgaatca gattcaagtct tcatttcagg 60
 cctcatactg cttctcccaag gtgcgttggaa gtctcataca gcagtgcaagg ggctggcg 120
 tcaccctgtc acacttccat gtatttattt gacacacac ttgttatacgg tcacttatct ggaccaatgg 180
 ttggggccta gggaaatgcc gccattctta ttgttatacgg tcacttatct ggaccaatgg 240
 atatacggtc acacatcaga ggaacagtgcg ataccagcta aaggaaaata tttcagaagg 300
 aaatgtgtcc ttgaccatag agaacactgt tttgggtgat ggtggccctt attgctgtgt 360
 agtggagata cctggagcgt tccatttgt ggactatatg ttggaaatgg aaccagaaat 420
 ttccacgggt ccaccaacaa ggcccacagg tacaggaaga cccacaacta tttcaacaag 480
 atccacacat gtacccaatc caaccagagt ctctacctt acttctccaa caccagcaca 540
 cacagagacc tacaaaccag aggccactac attttatcca gatcagacta cagctgaggt 600
 gacagaaacc ttacccctcta ctcctgcaga ctggcataac actgtgacat cctcagatga 660
 cccttggat gataacactg aagtaatccc tccacagaag ccacagaaaa acctgaataa 720
 gggcttctat gtggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780
 gtttatcacc agtacgtgg ttatggaaag gaagtcagaa tctctgagct tcgttgcctt 840
 ccctatctt aagattggag cttcccccaa aaaagtggc gaacggacca gatgtgaaga 900
 ccaggtctac attattgaag acactcctta ccccaagaa gagtcctagt gcctctac 958

<210> 9
 <211> 281
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(281)
 <223> TIM-3 BALB/c allele

<400> 9
 Met Phe Ser Gly Leu Thr Leu Asn Cys Val Leu Leu Leu Gln Leu
 1 5 10 15
 Leu Leu Ala Arg Ser Leu Glu Asp Gly Tyr Lys Val Glu Val Gly Lys
 20 25 30
 Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Pro Thr Ser Gly Thr Leu
 35 40 45
 Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
 50 55 60
 Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
 65 70 75 80
 Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
 85 90 95
 Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
 100 105 110
 Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
 115 120 125
 Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
 130 135 140
 Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
 145 150 155 160
 Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
 165 170 175
 Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
 180 185 190
 Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
 195 200 205
 Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys
 210 215 220
 Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
 225 230 235 240
 Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
 245 250 255
 Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr

260	265	270
Cys Tyr Val Asn Ser Gln Gln Pro Ser		
275	280	

<210> 10
<211> 2725
<212> DNA
<213> Mus musculus

<400> 10

```

ttttaaccga ggagctaaag ctatccctac acagagctgt ccttgattt cccctgcaa 60
gtactcatgt ttcaggctc taccctcaac tgggtctgc tgctgctgca actactactt 120
gcaaggcat tggaaagatgg ttataagggtt gagggtggta aaaatgccta tctgccctgc 180
agttacactc tacctacatc tgggacactt gtgcctatgt gctggggcaa gggattctgt 240
ccttggcac agtgtaccaa tgagttgctc agaactgtatg aaagaatgt gacatatacg 300
aaatccagca gataccagct aaaggcgat ctcaacaaag gagatgtgtc tctgatcata 360
aagaatgtga ctctggatga ccatggacc tactgctgca ggatacagtt ccctggctt 420
atgaatgata aaaaattaga actgaaatta gacatcaaag cagccaaggta cactccagct 480
cagactgccc atggggactc tactacagct tctccaagaa ccctaaccac ggagagaaat 540
ggttcagaga cacagacact ggtgaccctc cataataaca atgaaacaaa aatttccaca 600
tgggctgatg aaattaaggaa ctctggagaa acgatcagaa ctgctatcca cattggagt 660
ggagtcctg ctgggttgac cctggactt atcattgggt tcttaatccct taaatggtat 720
tcctgttaaga aaaaagaagt atcgagtttgc agccttattt cactggccaa cttgcctcca 780
ggagggttgg caaatgcagg agcagtcagg attcgctctg aggaaaatat ctacaccatc 840
gaggagaacg tatataaagt ggagaattca aatgagtaatc actgctacgt caacagccag 900
cagccatcct gaccgcctct ggactgccc ttttaaaggc tcgccttcat ttctgactt 960
ggtattttcc tttttgaaaaa ctatgtgata tgcacttgg caaccttattt ggaggttctg 1020
accacagcca ctgagaaaaag agttccagtt ttctggggat aattaactca caaggggatt 1080
cgactgtaac tcatgttaca ttgaaatgct ccattttatc cctgagtttcc agggatcgga 1140
tctcccaactc cagagacttc aatcatgcgt gttgaagctc actcgtgtt tcatacatat 1200
ggaatggta gtgtgtatgc ttttagacat agaggtttgt ggtatatccg caaagctcct 1260
gaacagtag gggaaataaa gggctaaatggat aggaagggtgc ggttctttgt tgatgttgaa 1320
aatctaaaga agttggtagc ttttcttagag atttctgacc ttgaaagatt aagaaaaaagc 1380
caggtggcat atgcttaaca cgatataact tgggaacctt aggcaggagg gtgataagtt 1440
caaggtcagc cagggtctatc ctggtaagac tgcctcaaaa tccaaagacg aaaataaaaca 1500
tagagacacg aggaggctgg agatgaggct cggacagtga ggtgcatttt gtacaagcac 1560
gaggaatcta tatttgcgt tagacccac atgaaaaagc taggccttggt agagcatgt 1620
tgttagactca agagatggag aggttaaaggc acaacagatc cccggggctt gcgtgcagtc 1680
agcttagcct aggtgtctgag ttccaagtcc acaagagttcc ctgtctcaaa gtaagatgg 1740
ctgagtatct ggcgaatgtc catgggggtt gtcctctgt ctcagaagag acatgcacat 1800
gaacctgcac acacacacac acacacacac acacacacac acacacacac acacatggaa 1860
tgaaggttct ctctgtgcct gctacccttc tataacatgt atctctacag gactctccct 1920
tgcctctgtt aagacatgag tgggagcatg gcagagcagt ccagtaatta attccagcac 1980
tcagaaggct ggagcagaag cgtggagagt tcaggagcac tgcctccaaactgcccagac 2040
tcttcttaca caagaaaaag gttacccgca agcagcctgc tgcgttgc tttttttttt 2100
gcgaaaaggca aactttgact gttgtgtctt caagggggac tgactcagac aacttctcca 2160
ttcctggagg aaactggagc tgggttttgc ttttttttttgc ttttttttttgc 2220
aggcagagct ctgcagcaat tctatatagt cagaaaaataa ttctttggta ggacagtcgt 2280
caccaatttgc ttttttttttgc ttttttttttgc ttttttttttgc 2340
agtgccttcgt atctgtgtctt gctcccatctt ataacagaat caaatttttttgc 2400
tgaaaaatattt aagtggtagc aatggtagct ttgttcaaaat ttttttttttgc 2460
aactgtgtac atcagaggac atctgttagt gaggacaccca aaacccgtgg taccgtttt 2520
tcatgtatgtt aatgggttgc ttttttttttgc ttttttttttgc 2580
taggtggta tggaaaggag accatctaaac aaaatccattt agagataaca gctctcatgc 2640
agaaggaaaaa actaatctca aatgtttttaa agtaataaaaaa ctgtactggc aaagtactttt 2700
gagcatattt aaaaaaaaaaaaaaaa 2725

```

<210> 11
<211> 281
<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(281)

<223> TIM-3, C.D2 ES-HBA and DBA/2J allele

<400> 11

Met Phe Ser Gly Leu Thr Leu Asn Cys Val Leu Leu Leu Gln Leu
1 5 10 15
Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys
20 25 30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
35 40 45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
50 55 60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65 70 75 80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
85 90 95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
100 105 110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
115 120 125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
130 135 140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145 150 155 160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
165 170 175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
180 185 190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
195 200 205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys
210 215 220
Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
225 230 235 240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
245 250 255
Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr
260 265 270
Cys Tyr Val Asn Ser Gln Gln Pro Ser
275 280

<210> 12

<211> 862

<212> DNA

<213> Mus musculus

<400> 12

ccctcccaa gtactcatgt tttcaggtct taccctcaac tgtgtcctgc tgctgctgca 60
actactactt gcaaggatcat tggaaaatgc ttatgtgtt gaggttggtt agaatgccta 120
tctgccctgc agttacactc tatctacacc tggggcactt gtgcctatgt gctggggcaa 180
gggattctgt ccttggtcac agtgtaccaa cgagttgctc agaactgatg aaagaaatgt 240
gacatatcag aaatccagca gataccagct aaagggcgat ctcaacaaag gagacgtgtc 300
tctgatcata aagaatgtga ctctggatga ccatgggacc tactgctgca ggatacagtt 360
ccctggctt atgaatgata aaaaattaga actgaaattha gacatcaaag cagccaaggt 420
cactccagct cagactgccc atggggactc tactacagct tctccaagaa ccctaaccac 480
ggagagaaat gttcagaga cacagacact ggtgaccctc cataataaca atgaaacaaa 540

aatttccaca tgggctgatg aaattaagga ctctggagaa acgatcagaa ctgcttatcca 600
 cattggagtg ggagtctctg ctgggttgcac cctggcactt atcattggtg tcttaatcct 660
 taaatggat tcctgttaga aaaagaagtt atcgagtttgc agccttatttta cactggccaa 720
 cttgcctcca ggagggttgg caaatgcagg agcagtcagg attcgctctg aggaaaaatata 780
 ctacaccatc gaggagaacg tatatgaagt ggagaattca aatgagttact actgctacgt 840
 caacagccag cagccatcct ga 862

<210> 13
 <211> 345
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(345)
 <223> TIM-4, BALB/c allele

<400> 13

Met	Ser	Lys	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Val	Thr	Glu	Leu	Trp	Trp
1				5					10					15	
Leu	Tyr	Leu	Ser	Lys	Ser	Pro	Ala	Ala	Ser	Glu	Asp	Thr	Ile	Ile	Gly
				20				25					30		
Phe	Leu	Gly	Gln	Pro	Val	Thr	Leu	Pro	Cys	His	Tyr	Leu	Ser	Trp	Ser
				35				40					45		
Gln	Ser	Arg	Asn	Ser	Met	Cys	Trp	Gly	Lys	Gly	Ser	Cys	Pro	Asn	Ser
				50				55				60			
Lys	Cys	Asn	Ala	Glu	Leu	Leu	Arg	Thr	Asp	Gly	Thr	Arg	Ile	Ile	Ser
				65			70			75			80		
Arg	Lys	Ser	Thr	Lys	Tyr	Thr	Leu	Leu	Gly	Lys	Val	Gln	Phe	Gly	Glu
				85				90					95		
Val	Ser	Leu	Thr	Ile	Ser	Asn	Thr	Asn	Arg	Gly	Asp	Ser	Gly	Val	Tyr
				100				105					110		
Cys	Cys	Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Lys	Asn
				115				120					125		
Val	Arg	Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr
				130			135				140				
Thr	Thr	Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu
				145			150			155			160		
Leu	Leu	Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr
				165				170					175		
Pro	Pro	Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr
				180				185					190		
Cys	Pro	Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly
				195				200					205		
Ser	Ala	Ile	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser
				210			215				220				
Gln	Arg	Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro
				225			230			235			240		
Thr	Gly	Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr
				245				250					255		
Gln	Lys	Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys
				260			265					270			
Ser	His	Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys
				275			280					285			
Val	Gly	Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Leu	Arg
				290			295				300				
Gly	Lys	Val	Thr	Gly	Ala	Asn	Cys	Leu	Gln	Arg	His	Lys	Arg	Pro	Asp
				305			310			315			320		
Asn	Thr	Glu	Val	Ser	Asp	Ser	Phe	Leu	Asn	Asp	Ile	Ser	His	Gly	Arg
				325				330					335		
Asp	Asp	Glu	Asp	Gly	Ile	Phe	Thr	Leu							

<210> 14
<211> 1032
<212> DNA
<213> Mus musculus

<400> 14
atgtccaagg ggcttctcct cctctggctg gtgacggagc tctggtggt ttatctgaca 60
ccagctgcct cagaggatac aataataggg tttttggccc agccggtgac tttgccttgt 120
cattacctct cggtgtccca gagccgcaac agtatgtgt gggccaaagg ttcatgtccc 180
aattccaaat gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
tcaacaaaat atacactttt ggggaagggtc cagtttgggt aagtgtcctt gaccatctca 300
aacaccaatc gaggtgacag tgggtgtac tgctgccgt a tagaggtgcc tggctgggtc 360
aatgtatgtca agaagaatgt ggcgttggag ctgaggagag ccacaacaac caaaaaaacc 420
acaacaacca cccggccaac caccacccct tatgttaacca ccaccacccc agagctgttt 480
ccaacaacag tcattgaccac atctgttctt ccaaccacca caccacccca gacactagcc 540
accactgcct tcattgtacagc agtgcaccacg tgccccctcaa caacacctgg ctccttctca 600
caagaaacca caaaagggtc cgccatcaact acagaatcaag aaactctgcc tgcatccaaat 660
cactctcaaa gaagcatgat gaccatatct acagacatag ccgtacttag gcccacaggc 720
tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
acaagttagt cttgcagaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
ttgatcatttgc cctgtgtgt gggatttggc ctaatgggtt tattgtttctt ggcgtttctc 900
cttcgaggga aagtccacagg agccaaactgt ttgcagagac acaagaggcc agacaacact 960
gaagatagt acacgcgtcctt caatgacatg tcacacggga gggatgatga agacgggatc 1020
ttcactctctt ga 1032

<210> 15
<211> 345
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(345)
<223> C.D2 ES-HBA and DBA/2J allele

<400> 15
Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Met Glu Leu Trp Trp
1 5 10 15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
20 25 30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
35 40 45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
50 55 60
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
65 70 75 80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
85 90 95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100 105 110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115 120 125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Lys Lys Pro Thr Thr
130 135 140
Thr Thr Arg Pro Thr Thr Pro Tyr Val Thr Thr Thr Pro Glu
145 150 155 160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr
165 170 175

Pro	Pro	Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr
															180
															185
Cys	Pro	Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly
															195
Ser	Ala	Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser
															210
															215
Gln	Arg	Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro
															225
Thr	Gly	Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr
															245
Gln	Lys	Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys
															260
Ser	His	Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys
															275
Val	Gly	Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Leu	Arg
															290
Gly	Lys	Val	Thr	Gly	Ala	Asn	Cys	Leu	Gln	Arg	His	Lys	Arg	Pro	Asp
															305
Asn	Thr	Glu	Val	Ser	Asp	Ser	Phe	Leu	Asn	Asp	Ile	Ser	His	Gly	Arg
															325
Asp	Asp	Glu	Asp	Gly	Ile	Phe	Thr	Leu							
															340
															345

<210> 16
<211> 1032
<212> DNA
<213> Mus musculus

<400> 16

atgtccaagg	ggcttctcct	cctctggctg	gtgatggagc	tctggtggt	ttatctgaca	60
ccagctgcct	cagaggatac	aataataggg	tttttggggc	agccggtgac	tttgccttgt	120
cattacctct	cgtggtccca	gagccgaac	agtatgtgt	ggggcaaagg	ttcatgtccc	180
aattccaagt	gcaatgcaga	gcttcgtccgt	acagatggaa	caagaatcat	ctccaggaag	240
tcaacaaaat	atacactttt	ggggaaaggc	cagtttgggt	aagtgtcctt	gaccatctca	300
aacaccaatc	gaggtgacag	tgggggtgtac	tgctgccgt	tagaggtgcc	tggctgggtc	360
aatgatgtca	agaagaatgt	gcgcttggag	ctgaggagag	ccacaacaac	caaaaaacca	420
acaacaacca	cccgcccaac	caccacccct	tatgttaacc	ccaccacccc	agagctgttt	480
ccaacaacag	tcatgaccac	atctgttctt	ccaaccacca	caccacccca	gacactagcc	540
accactgcct	tcagtagacgc	agtgaccacg	tgccccctcaa	caacacctgg	tcctttctca	600
caagaaacca	caaagggttc	cgccttcact	acagaatcag	aaactctgcc	tgcattcaat	660
cactctcaaa	gaagcatgat	gaccatatct	acagacatag	ccgtactcag	gcccacaggc	720
tctaaccctg	ggattctccc	atccacttca	cagctgacga	cacagaaaac	aacattaaca	780
acaagtgtgt	cttgccagaa	gacaactaaa	tcacatcaga	tcaacagcag	acagaccatc	840
ttgatcattg	cctgctgtgt	gggatttgg	ctaattgggt	tatttgttct	ggcgtttctc	900
cttcgaggg	aagtgcacagg	agccaactgt	ttgcagagac	acaagaggcc	agacaacact	960
gaagatagt	acagcgtcct	caatgacatg	tcacacggga	gggatgatga	agacgggatc	1020
ttcactctct	ga					1032

<210> 17
<211> 359
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(360)
<223> TIM-1 allele 1

<400> 17
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp

1	5	10	15
Ser	Val	Ala	Gly
Ser	Val	Lys	Val
20			25
Thr	Leu	Pro	Cys
		His	Tyr
		Ser	Gly
		Ala	Val
		Thr	Ser
		Met	Cys
		Trp	Asn
			35
			40
			45
Arg	Gly	Ser	Cys
Ser	Leu	Phe	Thr
		Cys	Gln
		Asn	Gly
		Ile	Val
		Trp	Thr
			50
			55
			60
Asn	Gly	Thr	His
Gly	Thr	His	Val
		Thr	Thr
		Tyr	Arg
		Lys	Asp
		Thr	Arg
		Tyr	Lys
		Leu	Leu
			65
			70
			75
			80
Gly	Asp	Leu	Ser
		Arg	Arg
		Asp	Val
		Ser	Leu
		Thr	Ile
		Glu	Asn
		Thr	Ala
			85
			90
			95
Val	Ser	Asp	Ser
		Gly	Val
		Tyr	Cys
		Cys	Arg
		Val	Glu
		His	Arg
		Gly	Trp
			100
			105
			110
Phe	Asn	Asp	Met
		Lys	Ile
		Thr	Val
		Ser	Leu
		Glu	Ile
		Val	Val
		Pro	Pro
		Lys	
			115
			120
			125
Val	Thr	Thr	Thr
		Pro	Ile
		Val	Thr
		Thr	Val
		Pro	Thr
		Thr	Val
		Thr	Thr
		Val	Val
			130
			135
			140
Arg	Thr	Ser	Thr
		Thr	Val
		Pro	Thr
		Thr	Thr
		Thr	Val
		Pro	Thr
		Thr	Thr
		Val	Val
			145
			150
			155
			160
Val	Pro	Thr	Thr
		Met	Ser
		Ile	Pro
		Thr	Thr
		Thr	Thr
		Val	Pro
			165
			170
			175
Met	Thr	Val	Ser
		Thr	Thr
		Ser	Val
		Pro	Thr
		Thr	Thr
		Ser	Ile
		Ile	Pro
			180
			185
			190
Thr	Thr	Thr	Ser
		Val	Pro
		Val	Thr
		Thr	Thr
		Val	Ser
		Thr	Phe
			195
			200
			205
Pro	Met	Pro	Leu
		Pro	Arg
		Gln	Asn
		His	Glu
		Pro	Val
		Ala	Thr
		Thr	Ser
		Pro	Pro
			210
			215
			220
Ser	Ser	Pro	Gln
		Pro	Ala
		Glu	Thr
		His	Pro
		Thr	Thr
		Leu	Gln
		Gly	Ala
			225
			230
			235
			240
Ile	Arg	Arg	Glu
		Pro	Thr
		Ser	Ser
		Pro	Leu
		Tyr	Tyr
		Ser	Tyr
		Tyr	Thr
		Asp	
			245
			250
			255
Gly	Asn	Asp	Thr
		Val	Thr
		Glu	Ser
		Ser	Asp
		Gly	Leu
		Leu	Trp
		Asn	Asn
		Asn	Asn
			260
			265
			270
Gln	Thr	Gln	Leu
		Leu	Phe
		Glu	Leu
		His	Ser
		Leu	Leu
		Thr	Ala
		Asn	Thr
		Thr	Thr
		275	
		280	
			285
Lys	Gly	Ile	Tyr
		Ala	Gly
		Val	Cys
		Ile	Ser
		Val	Leu
		Leu	Val
		Leu	Leu
		Ala	
			290
			295
			300
Leu	Leu	Gly	Val
		Ile	Ile
		Ala	Lys
		Lys	Tyr
		Tyr	Phe
		Phe	Lys
		Lys	Glu
			305
			310
			315
			320
Gln	Gln	Leu	Ser
		Val	Ser
		Phe	Ser
		Ser	Leu
		Gln	Ile
		Lys	Ala
		Ala	Leu
			325
			330
			335
Asn	Ala	Val	Glu
		Lys	Glu
		Val	Gln
		Ala	Glu
		Asp	Asn
		Ile	Tyr
		Tyr	Ile
		Glu	
			340
			345
			350
Asn	Ser	Leu	Tyr
		Ala	Thr
		Asp	
			355

<210> 18

<211> 1080

<212> DNA

<213> H. sapiens

<400> 18

atgcatcctc aagtggcat cttaagcctc atcctacatc tggcagattc ttagcttgt 60
tctgtaaagg ttggtgaga ggcagtcac tctgtcacac taccctgcca ctacagtgg 120
gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg caaaaatggc 180
attgtctgga ccaatggAAC ccacgtcacc tatcggaagg acacacgcta taagctattg 240
ggggacctt caagaaggGA tgtctttt accatagaaa atacagctgt gtctgacagt 300
ggcgtatatt gttgccgtgt tgagcaccgt gggtggttca atgacatgaa aatcaccgt 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tggccaacc 420
gtcacgactg ttcaaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480

gttccaaaca caatgagcat tccaaacgaca acgactgtc cgacgacaat gactgttca 540
 acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtgaca 600
 acaacggct ctaccttgc tcctccaatg ccttgccca ggcagaacca tgaaccagta 660
 gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
 ataaggagag aacccaccag ctcaccatt tactcttaca caacagatgg gaatgacacc 780
 gtgacagagt cttcagatgg ccttgaaat aacaatcaa ctcaactgtt cctagaacat 840
 agtctactga cgccaatac cactaaagga atctatgctg gagtctgtat ttctgtctg 900
 gtgcttcctg ctctttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggaggtt 960
 caacaactaa gtgttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
 aaggaagtcc aagcagaaga caatatctac attgagaata gtcttatgc cacggactaa 1080

<210> 19
 <211> 359
 <212> PRT
 <213> H. sapiens

 <220>
 <221> VARIANT
 <222> (1)...(359)
 <223> TIM-1, allele 2

<400> 19
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35 40 45
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50 55 60
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65 70 75 80
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85 90 95
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
 100 105 110
 Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
 115 120 125
 Val Thr Thr Pro Ile Val Thr Val Pro Thr Val Thr Thr Val
 130 135 140
 Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Thr Thr Thr
 145 150 155 160
 Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Val Pro Thr Thr
 165 170 175
 Met Thr Val Ser Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
 180 185 190
 Thr Thr Thr Ser Val Pro Val Thr Thr Ala Val Ser Thr Phe Val Pro
 195 200 205
 Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
 210 215 220
 Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala
 225 230 235 240
 Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
 245 250 255
 Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn
 260 265 270
 Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
 275 280 285
 Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala
 290 295 300

Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val
 305 310 315 320
 Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln
 325 330 335
 Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu
 340 345 350
 Asn Ser Leu Tyr Ala Thr Asp
 355

<210> 20
 <211> 1080
 <212> DNA
 <213> H. sapiens

<400> 20
 atgcatcctc aagtggcat cttaaggctc atcctacatc tggcagattc ttagctgg 60
 tctgtaaagg ttggggaga ggcaggtcca tctgtcacac tacccgtcca ctacagtgg 120
 gctgtcacat caatgtgctg gaataggggc tcatgttctc tattcacatg caaaaatggc 180
 attgtctgg acaatggaa ccacgtcacc tattcgaaagg acacacgcta taagctattg 240
 ggggacctt caagaaggga tgtctttt accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgt tgagcaccgt gggtggttca atgacatgaa aatcaccgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tggccaaacc 420
 gtcacgactg ttcaaacggg caccactgtt ccaacgacaa cgactgttcc aacgacaact 480
 gttccaacaa caatgagcat tccaaacgaca acgactgtc cgacgacaat gactgttca 540
 acgacaacga gcgttccaaac gacaacgagc attccaaacaa caacaagtgt tccagtgaca 600
 acagcgtct ctacctttgt tcctccaatg ctttgccca ggcagaacca tgaaccagta 660
 gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
 ataaggagag aacccaccag ctcaccattt tactcttaca caacagatgg gaatgacacc 780
 gtgacagagt cttcagatgg ctttggaaat aacaatcaa ctcaactgtt cctagaacat 840
 agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtctt 900
 gtgcttcttgc ctctttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggaggtt 960
 caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgaaaaa tgcagttgaa 1020
 aaggaagtcc aagcagaaga caatatctac attgagaata gtcttatgc cacggactaa 1080

<210> 21
 <211> 365
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(365)
 <223> TIM-1, allele 3

<400> 21
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35 40 45
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50 55 60
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65 70 75 80
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85 90 95
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
 100 105 110

Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
115							120					125			
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
130						135					140				
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Val	Pro	Met	Thr	Thr	
145					150				155				160		
Thr	Val	Pro	Thr	Thr	Thr	Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr
						165			170				175		
Thr	Thr	Val	Pro	Thr	Thr	Met	Thr	Val	Ser	Thr	Thr	Ser	Val	Pro	
						180			185			190			
Thr	Thr	Thr	Ser	Ile	Pro	Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Ala
						195			200			205			
Val	Ser	Thr	Phe	Val	Pro	Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu
						210		215			220				
Pro	Val	Ala	Thr	Ser	Pro	Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro
						225		230			235				240
Thr	Thr	Leu	Gln	Gly	Ala	Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu
						245			250			255			
Tyr	Ser	Tyr	Thr	Thr	Asp	Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp
							260		265			270			
Gly	Leu	Trp	Asn	Asn	Asn	Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu
						275			280			285			
Leu	Thr	Ala	Asn	Thr	Thr	Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser
						290		295			300				
Val	Leu	Val	Leu	Leu	Ala	Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr
							305		310			315			320
Phe	Phe	Lys	Lys	Glu	Val	Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu
							325			330			335		
Gln	Ile	Lys	Ala	Leu	Gln	Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu
							340		345			350			
Asp	Asn	Ile	Tyr	Ile	Glu	Asn	Ser	Leu	Tyr	Ala	Thr	Asp			
							355		360			365			

<210> 22
<211> 1098
<212> DNA
<213> *H. sapiens*

<400> 22
atgcatccctc aagtggtc cat cttaaaggcc tc atcctacatc tggcagattc tgttagcttgt 60
tctgtaaagg ttggtg gaga ggcagg tcca tctgtcacac taccctgcca ctacagt gga 120
gctgtcacat caatgtgctg gaatagaggc tc atggttctc tattcacatg caaaatg gc 180
atgtctgga ccaatggAAC ccacgtcacc tatcggaagg acacacgcta taagcttattg 240
ggggacctt caagaaggga tgc tctttt accatagaaa atacagctgt gtctgacagt 300
ggcgtatatt gttgccgtg tgagcaccgt ggg tgggttca atgacatgaa aatcaccgta 360
tcattggaga ttgtgccacc caaggtc acgt actactccaa ttgtcacaac tgg tccaaacc 420
gtcacgactg ttcaaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480
actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540
acgacaatga ctgttcaac gacaacgagc gttccaacgca caacgagcat tccaacaaca 600
acaagtgttc cagt gacaac arcgg tctct acctttgttc ctccaatgcc tttggcccagg 660
cagaaccatg aaccaggtagc cacttacca tcttccaccc agccagcaga aacccaccc 720
acgacactgc aggaggcaat aaggagagaa cccaccagct caccattgtt ctcttacaca 780
acagatggga atgacaccgt gacagagtct tca gatggcc tttggaaataa caatcaaact 840
caactgttcc tagaaacatag tctactgtacg gcaataccat ctaaaggaaat ctatgctgga 900
gtctgttattt ctgtcttgggt gcttcttgct ct tttgggttgc tcatcattgc caaaatgtt 960
ttcttcaaaa aggagggtca acaactaagt gttcatttgc gca gcttca aat taaatgtt 1020
ttgcaaaaatg cagg tggaaaa ggaagg tccaa gca gaaagaca atatctacat tgagaatagt 1080
ctttatgcca cggactaa 1098

<210> 23

<211> 359
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(359)
<223> TIM-1, allele 4

<400> 23
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1 5 10 15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20 25 30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35 40 45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50 55 60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65 70 75 80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85 90 95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100 105 110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115 120 125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130 135 140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Thr Thr Thr
145 150 155 160
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Val Pro Thr Thr
165 170 175
Met Thr Val Ser Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
180 185 190
Thr Thr Thr Ser Val Pro Val Thr Thr Ser Val Ser Thr Phe Val Pro
195 200 205
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
210 215 220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Thr
225 230 235 240
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
245 250 255
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Ser Asn Asn
260 265 270
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
275 280 285
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Ala
290 295 300
Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val
305 310 315 320
Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln
325 330 335
Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu
340 345 350
Asn Ser Leu Tyr Ala Thr Asp
355

<210> 24
<211> 1079
<212> DNA

<213> H. sapiens

<400> 24
atgcatcctc aagtggcat cttaagcctc atcctacatc tggcagattc ttagcttgt 60
tctgtaaagg ttgggaga ggcaggtcca tctgtcacac tacctgccatc acatgtgg 120
gctgtcacat caatgtctg gaatagaggc tcatgttctc tattcacatg caaaaatggc 180
attgtctgga ccaatggAAC ccacgtcacc tatacgaaAGG acacacgcta taagctattg 240
ggggaccttt caagaaggGA tgtcttttG accatagaaa atacagctgt gtctgacagt 300
ggcgtatatt gttgcgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
tcattggaga ttgtgccacc caaggtcactg actactccaa ttgtcacaac tggccaaacc 420
gtcacgactg ttcaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480
gttccaacaa caatgagcat tccaaacgaca acggactgtt ccgacgacaa tgactgttcc 540
aacgacaacg agcgttccaa cgacaacgag cattccaaca acaacaagtg ttccagtgac 600
aacatgtctc tacctttgtt cctccaaatgc ctttgcccag gcagaaccat gaaccagtag 660
ccacttcacc atcttcacct cagccagcag aaacccaccc tacgacactg cagggagcaa 720
taaggagaga acccaccaggc tcaccattgt actcttacac aacagatggg aatgacacccg 780
tgacagagtc tttagatggc ctttgarta acaatcaaac tcaactgttcc cttagaacata 840
gtctactgac ggcataatacc actaaaggaa tctatgttgg agtctgttatt tctgtcttgg 900
tgcttcttgc tcttttgggt gtcatcattt caaaaagata tttcttcaaa aaggagggttcc 960
aacaactaag tggcattt agcagccttc aaattaaagc tttgcaaaat gcagttgaaa 1020
aggaagtcca agcagaagac aatatctaca ttgagaatag tctttatgcc acggactaa 1079

<210> 25

<211> 364

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(364)

<223> TIM-1 allele 5

<400> 25

Met	His	Pro	Gln	Val	Val	Ile	Leu	Ser	Leu	Ile	Leu	His	Leu	Ala	Asp
1				5					10				15		
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Gly	Glu	Ala	Gly	Pro	Ser	Val
					20				25				30		
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn
						35			40				45		
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr
					50			55			60				
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu
					65			70			75			80	
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala
					85				90				95		
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp
					100				105				110		
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
					115			120			125				
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
					130			135			140				
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Val	Pro	Met	Thr	Thr	
					145			150			155			160	
Thr	Val	Pro	Thr	Thr	Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	
					165			170			175				
Thr	Thr	Val	Pro	Thr	Thr	Met	Thr	Val	Ser	Thr	Thr	Ser	Val	Pro	
					180			185			190				
Thr	Thr	Thr	Ser	Ile	Pro	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Val	
					195			200			205				
Ser	Thr	Phe	Val	Pro	Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro
					210			215			220				

Val Ala Thr Ser Pro Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr
 225 230 235 240
 Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr
 245 250 255
 Ser Tyr Thr Asp Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly
 260 265 270
 Leu Trp Asn Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu
 275 280 285
 Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val
 290 295 300
 Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe
 305 310 315 320
 Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln
 325 330 335
 Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp
 340 345 350
 Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp
 355 360

<210> 26
 <211> 1095
 <212> DNA
 <213> H. sapiens

<400> 26
 atgcatcctc aagtggcat cttaagcctc atcctacatc tggcagattc ttagctgg 60
 tctgtaaagg ttggggaga ggcagtcac tctgtcacac taccgtccca ctacagtgg 120
 gctgtcacat caatgtgctg gaatagaggg tcatgttctc tattcacatg ccaaatggc 180
 attgtctggc ccaatggAAC ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggacctt caagaaggga tgtctttt accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcaccgt gggtggttca atgacatgaa aatcaccgt 360
 tcattggaga ttgtgccacc caaggtcacc actactccaa ttgtcacaac tggccaacc 420
 gtcacgactg ttcaaacggc caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480
 actgttccaa cgacaactgt tccaaacaaca atgagcattc caacgacaac gactgttccg 540
 acgacaatga ctgttcaac gacaacggc gttccaacga caacgagcat tccaaacaaca 600
 agtgttccag tgacaacaac ggtcttacc ttgttccctc caatgcctt gcccaggcag 660
 aaccatggAAC cagtagccac ttcaaccatct tcacctcagc cagcagaaac ccaccctacg 720
 acactgcagg gagcaataag gagagaaccc accagctcac cattgtactc ttacacaaca 780
 gatggaaatg acaccgtgac agagtttca gatggcctt ggaataacaa tcaaactcaa 840
 ctgttccctag aacatagtct actgacggcc aataccacta aaggaatcta tgctggagtc 900
 tgtatttctg tcttggtgct tcttgcctt ttgggtgtca tcattgccaa aaagtatttc 960
 ttcaaaaagg agttcaaca actaagtgtt tcatttagca gccttcaaatt taaagctttg 1020
 caaaatgcag ttgaaaaggag agtccaaagca gaagacaata tctacattga gaatagtctt 1080
 tatgccacgg actaa 1095

<210> 27
 <211> 364
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(364)
 <223> TIM-1, allele 6

<400> 27
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30

Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35 40 45
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50 55 60
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65 70 75 80
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85 90 95
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
 100 105 110
 Phe Asn Asp Met Lys Ile Thr Val Ser Leu Gly Ile Val Pro Pro Lys
 115 120 125
 Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
 130 135 140
 Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Met Thr Thr
 145 150 155 160
 Thr Val Pro Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
 165 170 175
 Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Ser Val Pro
 180 185 190
 Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Val
 195 200 205
 Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro
 210 215 220
 Val Ala Thr Ser Pro Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr
 225 230 235 240
 Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr
 245 250 255
 Ser Tyr Thr Thr Asp Gly Asp Asp Thr Val Thr Glu Ser Ser Asp Gly
 260 265 270
 Leu Trp Asn Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu
 275 280 285
 Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val
 290 295 300
 Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe
 305 310 315 320
 Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln
 325 330 335
 Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp
 340 345 350
 Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp
 355 360

<210> 28
 <211> 1099
 <212> DNA
 <213> H. sapiens

<400> 28
 atgcatcctc aagtggcat cttaagcctc atcctacatc tggcagattc ttagcttgt 60
 tctgtaaagg ttggggaga ggcaggtcca tctgtcacac taccctgcca ctacagtgg 120
 gctgtcacat caatgtctg gaatagaggc tcatagttctc tattcacatg caaaaatggc 180
 attgtctgga ccaatggAAC ccacgtcacc tatcgaaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctttt accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcaccgt gggtggttca atgacatgaa aatcaccgt 360
 tcattggaga ttgtggcacc caaggtcacg actactccaa ttgtcacaac tggccaacc 420
 gtcacgactg ttcaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacc 480
 gactgttcca acgacaactg ttccaacaac aatgagcatt ccaacgacaa cgactgttcc 540
 gacgacaatg actgtttcaa cgacaacgag ctttccaaacg acaacgagca ttccaacaac 600
 aacaagtgtt ccagtacaa caacgtctc tacctttgtt ctttccaaatgc ctttgcccag 660

gcagaaccat gaaccagtag ccacttcacc atcttcaccc cagccagcag aaacccaccc 720
tacgacactg caggagcaa taaggagaga acccaccagg tcaccattgt actcttacac 780
aacagatggg gatgacaccg tgacagagtc ttcatatgc ctttgaata acaatcaaa 840
tcaactgttc ctagaacata gtctactgac gccaaatacc actaaaggaa tctatgtgg 900
agtctgtatt tctgtcttg tgcttcttc tctttgggt gtcatttcattt agcagccttc aaatcaaagc 960
tttcttcaaa aaggaggttc aacaactaag tgtttcattt agcagccttc aaatcaaagc 1020
tttgcaaaat gcagttgaaa aggaagtcca agcagaagac aatatctaca ttgagaatag 1080
tctttatgcc acggactaa 1099

<210> 29
<211> 301
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(301)
<223> TIM-3, allele 1

<400> 29
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
1 5 10 15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50 55 60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85 90 95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100 105 110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115 120 125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
130 135 140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145 150 155 160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165 170 175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
180 185 190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
195 200 205
Ile Cys Ala Gly Leu Ala Leu Ala Ile Phe Gly Ala Leu Ile Phe
210 215 220
Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
225 230 235 240
Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
245 250 255
Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
260 265 270
Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
275 280 285
Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
290 295 300

<210> 30

<211> 1116
<212> DNA
<213> H. sapiens

<400> 30
ggagaggtaa aactgtgcct aacagaggta tcctctgact tttcttctgc aagctccatg 60
ttttcacatc ttccctttga ctgtgcctg ctgctgctgc tgctactact tacaagggcc 120
tcagaagtgg aatacagagc ggaggcggt cagaatgcct atctgcctg cttctacacc 180
ccagccccc cagggAACCT cgtgcggcgc tgctggggca aaggaggcctg tcctgtgttt 240
aatgtggca acgtggcgct caggactgat gaaaggatg tgaattattg gacatccaga 300
tactggctaa atggggattt ccgcaaaggaa gatgtgtccc tgaccataga gaatgtgact 360
ctagcagaca gtgggatctia ctgctgcgg atccaaatcc caggcataat gaatgtgaa 420
aaatttaacc tgaagtttgtt catcaaacca gccaaggcga cccctgcacc gactctgcag 480
agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg cccagcagag 540
acacagacac tggggagcct ccctgatata aatctaacad aaatatccac attggccaa 600
gagttacggg actcttagatt ggc当地atgac ttacgggact ctggagcaac catcagaata 660
ggcatctaca tcggagcagg gatctgtct gggctggctc tggctcttat cttcggcgct 720
ttaatttca aatggtattt tcatacgaaa gagaagatac agaatttaag cctcatctct 780
ttggccaaacc tccctccctc aggatggca aatgcagtag cagagggat tcgctcagaa 840
gaaaacatct ataccattga agagaacgta tatgaagtgg aggagccaa tgagtattat 900
tgctatgtca gcagcaggca gcaaccctca caacctttgg gttgtcgctt tgcaatgcca 960
tagatccaac caccttattt ttgagcttgg tttttgtct tttcagaaa ctatgagctg 1020
tgtcacctga ctgggtttgg aggttctgtc cactgctatg gagcagagtt ttcccatttt 1080
cagaagataa tgactcacat gggaaattgaa ctggga 1116

<210> 31
<211> 301
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(301)
<223> TIM-3, allele 2

<400> 31
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
1 5 10 15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50 55 60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85 90 95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100 105 110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115 120 125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe
130 135 140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145 150 155 160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165 170 175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
180 185 190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly

195	200	205	
Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe	Gly Ala Leu Ile Phe		
210	215	220	
Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn	Leu Ser Leu Ile		
225	230	235	240
Ser Leu Ala Asn Leu Pro Pro Ser Gly	Leu Ala Asn Ala Val	Ala Glu	
245	250	255	
Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile	Glu Glu Asn Val Tyr		
260	265	270	
Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr	Val Ser Ser Arg Gln		
275	280	285	
Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala	Met Pro		
290	295	300	

<210> 32

<211> 1116

<212> DNA

<213> H. sapiens

<400> 32

```

ggagagttaa aactgtgcct aacagagggtg tcctctgact tttcttctgc aagctccatg 60
ttttcacatc ttccctttga ctgtgtcctg ctgctgctgc tgctactact tacaagggtcc 120
tcagaagtgg aatacagagc ggaggtcggt cagaatgcct atctgccctg cttctacacc 180
ccagccccc cagggAACCT cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240
gaatgtggca acgtgggtc caggactgat gaaagggtat tgaattattt gacatccaga 300
tactggctaa atggggattt ccgcaagga gatgtgtccc tgaccataga gaatgtgact 360
ctagcagaca gtgggatcta ctgctccgg atccaaatcc caggcataat gaatgatgaa 420
aaatttaacc tgaagttggc catcaaacc cccaagggtca cccctgcacc gactcggcag 480
agagacttca ctgcagcctt tccaaggatg cttaccacca gggacatgg cccagcagag 540
acacagacac tggggagcct ccctgatata aatctaacc aatatccac attggccaat 600
gagttacggg actctagatt ggccaatgac ttacgggact ctggagcaac catcagaata 660
ggcatctaca tcggagcagg gatctgtct gggctggctc tggctttat cttcggcgct 720
ttaatttca aatggtattt tcatacgaaa gagaagatac agaatttaag cctcatct 780
ttggccaaacc tccctccctc aggattggca aatgcagtag cagagggat tcgctcagaa 840
gaaaacatct ataccattga agagaacgtt tatgaagtgg aggagccaa tgagtattat 900
tgctatgtca gcagcaggca gcaaccctca caacctttgg gttgtcgctt tgcaatgcca 960
tagatccaac caccttattt ttgagcttgg tttttgtct ttttcagaaa ctatgagctg 1020
tgtcacctga ctggtttgg aggttctgtc cactgctatg gagcagagtt ttcccattt 1080
cagaagataa tgactcacat gggaaattgaa ctggga 1116

```

<210> 33

<211> 378

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(378)

<223> TIM-4, allele 1

<400> 33

Met Ser Lys Glu Pro Leu Ile Leu Trp	Leu Met Ile Glu Phe Trp Trp		
1	5	10	15
Leu Tyr Leu Thr Pro Val Thr Ser Glu	Thr Val Val Thr Glu Val Leu		
20	25	30	
Gly His Arg Val Thr Leu Pro Cys	Leu Tyr Ser Ser Trp Ser His Asn		
35	40	45	
Ser Asn Ser Met Cys Trp Gly	Lys Asp Gln Cys Pro Tyr Ser Gly Cys		
50	55	60	
Lys Glu Ala Leu Ile Arg Thr Asp	Gly Met Arg Val Thr Ser Arg Lys		

65	70	75	80
Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser			
85	90	95	
Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys			
100	105	110	
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg			
115	120	125	
Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr			
130	135	140	
Thr Thr Arg Arg Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln Met			
145	150	155	160
Thr Thr Thr Pro Ala Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp			
165	170	175	
Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr			
180	185	190	
Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu			
195	200	205	
Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu			
210	215	220	
Thr Ala Glu Ser Glu Thr Val Leu Pro Ser Asp Ser Trp Ser Ser Ala			
225	230	235	240
Glu Ser Thr Ser Ala Asp Thr Val Leu Leu Thr Ser Lys Glu Ser Lys			
245	250	255	
Val Trp Asp Leu Pro Ser Thr Ser His Val Ser Met Trp Lys Thr Ser			
260	265	270	
Asp Ser Val Ser Ser Pro Gln Pro Gly Ala Ser Asp Thr Ala Val Pro			
275	280	285	
Glu Gln Asn Lys Thr Thr Lys Thr Gly Gln Met Asp Gly Ile Pro Met			
290	295	300	
Ser Met Lys Asn Glu Met Pro Ile Ser Gln Leu Leu Met Ile Ile Ala			
305	310	315	320
Pro Ser Leu Gly Phe Val Leu Phe Ala Leu Phe Val Ala Phe Leu Leu			
325	330	335	
Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser Gln Lys His Thr Arg Leu			
340	345	350	
Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly			
355	360	365	
Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu			
370	375		

<210> 34
 <211> 1156
 <212> DNA
 <213> H. sapiens

<400> 34
 atgtccaaag aacctctcat tctctggctg atgattgagt tttggtggt ttacctgaca 60
 ccagtcaattt cagagactgt tggcggag gttttgggtc accgggtgac tttgcctgt 120
 ctgtactcat cctggtctca caacagcaac agcatgtgtct gggggaaaga ccagtgc 180
 tactccggtt gcaaggaggg cgtcatccgc actgtatggaa tgagggtgac ctcaagaaag 240
 tcagaaaaat atagacttca ggggactatac ccgagagggtg atgtctccctt gaccatctta 300
 aaccccagtg aaagtgacag cggtgtgtac tgctgccgca tagaagtgcc tggctgggtc 360
 aacgatgtaa agataaacgt gcgcctgaat ctacagagag cctcaacaac cacgcac 420
 acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaaatg 480
 acaacaaccc cagctgcact tccaacaaca gtcgtgacca caccgatct cacaaccgga 540
 acaccactcc agatgacaac cattggcgac ttccacaacag caaacacgtg cctttcacta 600
 accccaagca cccttccgga ggaagccaca ggtttctga ctcccgagcc ttctaaggaa 660
 gggcccatcc tcactgcaga atcagaaaact gtcctccccca gtgattcctg gagtagtgc 720
 gagtctactt ctgctgacac tggctggctg acatccaaag agtccaaagt ttggatctc 780
 ccatcaacat cccacgtgtc aatgtggaaa acgagtgatt ctgtgtcttc tcctcagcct 840

ggagcatctg atacaggcagt tcctgaggcag aacaaaacaa caaaaaacagg acagatggat 900
 ggaataccca tgtcaatgaa gaatgaaatg cccatctccc aactactgtat gatcatcgcc 960
 ccctccttgg gatttgtgct ctgcgcattt tttgtggcgt ttctcctgag agggaaactc 1020
 atggaaacct attgttcgca gaaacacaca aggcttagact acatggaga tagtaaaaat 1080
 gtcctcaatg acgtgcagca tggaaaggaa gacgaagacg gccttttac cctctaacaa 1140
 cgcagtagca tgtag 1156

<210> 35

<211> 378

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(378)

<223> TIM-4, allele 2

<400> 35

Met	Ser	Lys	Glu	Pro	Leu	Ile	Leu	Trp	Leu	Met	Ile	Glu	Phe	Trp	Trp
1										10					15
Leu	Tyr	Leu	Thr	Pro	Val	Thr	Ser	Glu	Thr	Val	Val	Thr	Glu	Val	Leu
										20		25			30
Gly	His	Arg	Val	Thr	Leu	Pro	Cys	Leu	Tyr	Ser	Ser	Trp	Ser	His	Asn
										35		40			45
Ser	Asn	Ser	Met	Cys	Trp	Gly	Lys	Asp	Gln	Cys	Pro	Tyr	Ser	Gly	Cys
										50		55			60
Lys	Glu	Ala	Leu	Ile	Arg	Thr	Asp	Gly	Met	Arg	Val	Thr	Ser	Arg	Lys
										65		70			80
Ser	Ala	Lys	Tyr	Arg	Leu	Gln	Gly	Thr	Ile	Pro	Arg	Gly	Asp	Val	Ser
										85		90			95
Leu	Thr	Ile	Leu	Asn	Pro	Ser	Glu	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys
										100		105			110
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Ile	Asn	Val	Arg
										115		120			125
Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr	Thr	Thr	His	Arg	Thr	Ala	Thr	Thr
										130		135			140
Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr	Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met
										145		150			160
Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro	Thr	Thr	Val	Val	Thr	Thr	Pro	Asp
										165		170			175
Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln	Met	Thr	Thr	Ile	Ala	Val	Phe	Thr
										180		185			190
Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu	Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu
										195		200			205
Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu	Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu
										210		215			220
Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu	Pro	Ser	Asp	Ser	Trp	Ser	Ser	Val
										225		230			240
Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val	Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys
										245		250			255
Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser	His	Val	Ser	Met	Trp	Lys	Thr	Ser
										260		265			270
Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro	Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro
										275		280			285
Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr	Gly	Gln	Met	Asp	Gly	Ile	Pro	Met
										290		295			300
Ser	Met	Lys	Asn	Glu	Met	Pro	Ile	Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala
										305		310			320
Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe	Ala	Leu	Phe	Val	Ala	Phe	Leu	Leu
										325		330			335
Arg	Gly	Lys	Leu	Met	Glu	Thr	Tyr	Cys	Ser	Gln	Lys	His	Thr	Arg	Leu

340	345	350
Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly		
355	360	365
Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu	.	
370	375	

<210> 36
<211> 1156
<212> DNA
<213> H. sapiens

<400> 36

atgtccaaag aacctctcat tctctggctg atgattgagt tttggtggct ttacctgaca 60
ccagtcactt cagagactgt tgtgacggag gttttgggtc accgggtgac ttgcgcctgt 120
ctgtactcat cctggtctca caacagcaac agcatgtgct gggggaaaaga ccagtgcccc 180
tactccggtt gcaaggaggc gctcatccgc actgatggaa tgagggtgac ctcaagaaaag 240
tcagcaaaat atagacttca ggggactatac ccgagagggtg atgttcctt gaccatctta 300
aacccccagt aaagtgacag cggtgtgtac tgctgccga tagaagtgcc tggctgggtc 360
aacgatgtaa agataaacgt gcgcctgaat ctacagagag cctcaacaac cacgcacaga 420
acagcaacca ccaccacacg cagaacaaca acaaacaagcc ccaccaccac ccgacaaaatg 480
acaacaaccc cagtcgact tccaacaaca gtcgtgacca caccgcatac cacaaccgga 540
acaccactcc agatgacaac cattggcgtc ttccacaacag caaacacgtg ccttcacta 600
accccaagca cccttccgga ggaagccaca ggtttctga ctcccgagcc ttctaaggaa 660
gggccccatcc tcactgcaga atcagaaaact gtcctccca gtgattcctg gagtagtgtt 720
gagttctactt ctgtgacac tgcgtgtctg acatccaaag agtccaaagt ttgggatctc 780
ccatcaacat cccacgtgtc aatgtggaaa acgagtgatt ctgtgtcttc tcctcagcct 840
ggagcatctg atacagcagt tcctgacgcg aacaaaacaa caaaaacagg acagatggat 900
ggaataaccca tgtcaatgaa gaatgaaatg cccatctccc aactactgtat gatcatcgcc 960
ccctccttgg gatttgtctt cttcgcatgt tttgtggcgt ttctcctgag agggaaaactc 1020
atggaaacctt attgttcgca gaaacacacaa aggctagact acattggaga tagtaaaaat 1080
gtcctcaatg acgtgcagca tggaaaggaa gacgaagacg gccttttac cctctaacaa 1140
cgcagtagca tqtag 1156

<210> 37
<211> 481
<212> DNA
<213> *H. sapiens*

```
<220>
<221> exon
<222> (152)...(430)
<223> Exon 3, reference sequence
```

```
<400> 37
ttcttagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
ctgtcattgg tgtgctaggg tacagttcca gcctgaggtctt gtttgactta 120
tgctcacctt catgttgcatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
actgttccaa ccgtcacgac tggtcgaaacg agcaccactg ttccaacgac aacgactgtt 240
ccaacgacaa ctgttccaaac aacaatgagc attccaacgca caacgactgt tctgacgaca 300
atgactgttt caacgacaaac gagcgttcca acgacaacgca gcattccaac aacaacaagt 360
gttccagtgaa cacaactgtt ctctacccccc gttcctccaa tgccttgcc cagggcagaac 420
catgaaccagg taaaacaga tgtgttggaa agccccaaagg ccttctaatttggaggactg 480
g
```

<210> 38
<211> 499
<212> DNA
<213> *H. sapiens*

<220>

<221> exon
 <222> (152)...(448)
 <223> Exon 3, INS157 polymorphism

<400> 38
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tttgttaggg tacagttcca gcctgaggct cttgttttctt gtttgactta 120
 tgctcaactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgttccaa ccgtcacgac ttttgcgaacg agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
 acgactgttc tgacgacaat gactgttca acgacaacga gcgttccaac gacaacgagc 360
 attccaacaa caacaagtgt tccagtgaca acaactgtct ctacctttgt tcctccaatg 420
 ccttgcacca ggcagaacca tgaaccaggtaaaa aacgatgtt gtttggaaag cccaaaggcc 480
 ttctaattgag gagctgcgg 499

<210> 39
 <211> 496
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(445)
 <223> Exon 3, 195delt polymorphism

<400> 39
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tttgttaggg tacagttcca gcctgaggct cttgttttctt gtttgactta 120
 tgctcaactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgttccaa ccgtcacgac ttttgcgaacg agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
 acgactgttc tgacgacaat gactgttca acgacaacga gcgttccaac gacaacgagc 360
 attccaacaa caagtgttcc agtgacaaca actgtctcta ctttgcacca tccaatgcct 420
 ttgcccaggc agaaccatga accaggtaaa acagatgtt gtttggaaagccc aaaggccttc 480
 taatgaggag ctgcgg 496

<210> 40
 <211> 496
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(445)
 <223> Exon 3, 157insMTTVP polymorphism

<400> 40
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tttgttaggg tacagttcca gcctgaggct cttgttttctt gtttgactta 120
 tgctcaactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgttccaa ccgtcacgac ttttgcgaacg agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacga ctgttccaaac gacaactgtt ccaacaacaa tgagcattcc aacgacaacg 300
 actgttctga cgacaatgac ttttcaacg acaacgagcg ttccaacgac aacgagcatt 360
 ccaacaacaa caagtgttcc agtgacaaca actgtctcta ctttgcacca tccaatgcct 420
 ttgcccaggc agaaccatga accaggtaaa acagatgtt gtttggaaagccc aaaggccttc 480
 taatgaggag ctgcgg 496

<210> 41
 <211> 18
 <212> DNA

<213> H. sapiens	
<400> 41	
gtgtctgaca gtggcgta	18
<210> 42	
<211> 18	
<212> DNA	
<213> H. sapiens	
<400> 42	
tttgcgcagg cagaacca	18
<210> 43	
<211> 18	
<212> DNA	
<213> H. sapiens	
<400> 43	
ccacccaagg tcacgact	18
<210> 44	
<211> 18	
<212> DNA	
<213> H. sapiens	
<400> 44	
atgccacgga ctaagacc	18
<210> 45	
<211> 41	
<212> DNA	
<213> H. sapiens	
<400> 45	
ggaattcgtc gaccaccatg catcctaag tggtcatctt a	41
<210> 46	
<211> 42	
<212> DNA	
<213> H. sapiens	
<400> 46	
ggaattcgtcg gccgctcatt agtccgtggc ataaacagta tt	42
<210> 47	
<211> 20	
<212> DNA	
<213> H. sapiens	
<400> 47	
tcaagtggtc atcttaagcc	20
<210> 48	
<211> 22	
<212> DNA	
<213> H. sapiens	
<400> 48	
taaactctca aagagcacca ct	22

<210> 49	
<211> 22	
<212> DNA	
<213> H. sapiens	
<400> 49	
acagactcca gcatagattc ct	22
<210> 50	
<211> 22	
<212> DNA	
<213> H. sapiens	
<400> 50	
gcaccaagac agaaatacag ac	22
<210> 51	
<211> 31	
<212> DNA	
<213> H. sapiens	
<400> 51	
agaaggcaccc aagacagaaa tacagactcc a	31
<210> 52	
<211> 19	
<212> DNA	
<213> H. sapiens	
<400> 52	
ttcttagctgg gcaatgacc	19
<210> 53	
<211> 20	
<212> DNA	
<213> H. sapiens	
<400> 53	
ccgcagctcc tcattagaag	20